

SEQUENCE LISTING

<110> GARGER, Stephen A.
TURPEN, Thomas H.
KUMAGAI, Monto H.

<120> PRODUCTION OF LYSOSOMAL ENZYMES IN
PLANTS BY TRANSIENT EXPRESSION

<130> 008010087CPUS06

<140> To Be Assigned

<141> 2001-11-13

<160> 37

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<211> 15

<212> PRT

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<212> PRT

<213> Homo sapiens

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<212> DNA

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<220>

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Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu			
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cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc			192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile			
50	55	60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc			240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly			
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tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg			288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met			
85	90	95	
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Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg			
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Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly			
115	120	125	
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Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly			
130	135	140	
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Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser			
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Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn			
180	185	190	
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His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys			
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Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala	
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Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser	
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Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn	
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tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag	1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln	
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 <213> Homo sapiens

<400> 4

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Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu	Arg
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Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile	Ser
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Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly	Trp
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Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met	Ala
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Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly	Leu
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Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met	Trp
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Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn	His
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Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn	Gln
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Gln	Leu	Leu	Pro	Val	Lys	Arg	Lys	Leu	Gly	Phe	Tyr	Glu	Trp	Thr	Ser
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Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu	Gln	Leu
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 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
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gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag 144
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc 192
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
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 85 90 95

gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc 336
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110

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 115 120 125

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 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140

ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct 480
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160

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 Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

cta gaa aac aca atg cag atg tct tta aaa gac tta ctt tct gaa aag 1296
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<210> 6
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 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240
 Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val

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      275              280              285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
      290              295              300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
      305              310              315              320
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
      325              330              335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
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Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
      355              360              365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
      370              375              380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
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Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
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Asp Glu Leu
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
      20              25              30

gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag      144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
      35              40              45

cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc      192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
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agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc      240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly

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gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc				336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	100	105	110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga				384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	115	120	125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc				432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	130	135	140	
ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct				480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	145	150	155	160
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt				528
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	165	170	175	
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Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	180	185	190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg				624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	195	200	205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat				672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	210	215	220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag				720
His Trp Arg Asn Phe Ala Asp Ile Asp Ser Trp Lys Ser Ile Lys	225	230	235	240
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Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val	245	250	255	
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac				816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn	260	265	270	
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Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala	275	280	285	

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 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300

cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat 960
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

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 325 330 335

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 Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala

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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
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gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
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Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
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Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
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Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
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Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	
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Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	
180 185 190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	
195 200 205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	

210	215	220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag			720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys			
225	230	235	240
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt			768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val			
245	250	255	
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac			816
Ala Gly Pro Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn			
260	265	270	
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct			864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala			
275	280	285	
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc			912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser			
290	295	300	
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat			960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn			
305	310	315	320
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac			1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn			
325	330	335	
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct			1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala			
340	345	350	
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca			1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala			
355	360	365	
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc			1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile			
370	375	380	
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act			1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
385	390	395	400
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
405	410	415	
cta gaa aac aca atg cag atg tct tta tct gaa aag gac gaa tta tga			1296
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420	425	430	

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 <211> 431
 <212> PRT
 <213> Homo sapiens

<400> 10

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Arg	Phe	Leu	Ala	Leu	Val	Ser	Trp	Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu
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Asp	Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
		35						40				45			
Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
		50				55					60				
Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
					70						75			80	
Trp	Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
				85					90				95		
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
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Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
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Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
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Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
		145			150					155				160	
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
				165					170					175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
		180						185					190		
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
		195					200					205			
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
		210				215					220				
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys
		225			230					235				240	
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
			245						250					255	
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
		260					265					270			
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
		275					280					285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
		290				295					300				
Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
		305			310					315				320	
Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
			325						330					335	
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
		340					345						350		
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala
		355					360					365			
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile

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      370              375              380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385              390              395              400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
      405              410              415
Leu Glu Asn Thr Met Gln Met Ser Leu Ser Glu Lys Asp Glu Leu
      420              425              430

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<210> 11
<211> 1266
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(1266)

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cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg      96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
      20              25              30

gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag      144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
      35              40              45

cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc      192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
      50              55              60

agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc      240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
      65              70              75

tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg      288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
      85              90              95

gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc      336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
      100              105              110

ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga      384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
      115              120              125

ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc      432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
      130              135              140

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ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala 145 150 155 160	480
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser 165 170 175	528
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn 180 185 190	576
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met 195 200 205	624
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn 210 215 220	672
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys 225 230 235 240	720
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val 245 250 255	768
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn 260 265 270	816
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala 275 280 285	864
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser 290 295 300	912
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn 305 310 315 320	960
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn 325 330 335	1008
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala 340 345 350	1056
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala	1104

355

360

365

gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc 1152
 Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

aca cag ctg ctg cct gtg aaa agg aag cta ggg ttc tat gaa tgg act 1200
 Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Thr Glu Trp Thr
 385 390 395 400

tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag 1248
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 405 410 415

cta gaa aac aca atg taa 1266
 Leu Glu Asn Thr Met *
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<211> 421

<212> PRT

<213> Homo sapiens

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 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys

225 230 235 240
 Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255
 Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270
 Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320
 Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335
 Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350
 Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365
 Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380
 Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
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 Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415
 Leu Glu Asn Thr Met
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<210> 13

<211> 1284

<212> DNA

<213> Homo sapiens

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cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg 96
 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30

gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag 144
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc 192
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60

agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc 240
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly

65	70	75	80	
tgg aag gat gca ggt	tat gag tac ctc	tgc att gat gac tgt	tgg atg	288
Trp Lys Asp Ala Gly	Tyr Glu Tyr Leu	Cys Ile Asp Asp Cys	Trp Met	
85	90	95		
gct ccc caa aga gat	tca gaa ggc aga	ctt cag gca gac	cct cag cgc	336
Ala Pro Gln Arg Asp	Ser Glu Gly Arg	Leu Gln Ala Asp	Pro Gln Arg	
100	105	110		
ttt cct cat ggg att	cgc cag cta gct	aat tat gtt cac	agc aaa gga	384
Phe Pro His Gly Ile	Arg Gln Leu Ala	Asn Tyr Val His	Ser Lys Gly	
115	120	125		
ctg aag cta ggg att	tat gca gat gtt	gga aat aaa acc	tgc gca ggc	432
Leu Lys Leu Gly Ile	Tyr Ala Asp Val	Gly Asn Lys Thr	Cys Ala Gly	
130	135	140		
ttc cct ggg agt ttt	gga tac tac gac	att gat gcc cag	acc ttt gct	480
Phe Pro Gly Ser Phe	Gly Tyr Tyr Asp	Ile Asp Ala Gln	Thr Phe Ala	
145	150	155	160	
gac tgg gga gta gat	ctg cta aaa ttt	gat ggt tgt tac	tgt gac agt	528
Asp Trp Gly Val Asp	Leu Leu Lys Phe	Asp Gly Cys Tyr	Cys Asp Ser	
165	170	175		
ttg gaa aat ttg	gca gat ggt tat	aag cac atg tcc	ttg gcc ctg aat	576
Leu Glu Asn Leu Ala	Asp Gly Tyr Lys	His Met Ser Leu	Ala Leu Asn	
180	185	190		
agg act ggc aga	agc att gtg tac	tcc tgt gag tgg	cct ctt tat atg	624
Arg Thr Gly Arg Ser	Ile Val Tyr Ser	Cys Glu Trp Pro	Leu Tyr Met	
195	200	205		
tgg ccc ttt caa aag	ccc aat tat aca	gaa atc cga cag	tac tgc aat	672
Trp Pro Phe Gln Lys	Pro Asn Tyr Thr	Glu Ile Arg Gln	Tyr Cys Asn	
210	215	220		
cac tgg cga aat ttt	gct gac att gat	gat tcc tgg aaa	agt ata aag	720
His Trp Arg Asn Phe	Ala Asp Ile Asp	Asp Ser Trp Lys	Ser Ile Lys	
225	230	235	240	
agt atc ttg gac tgg	aca tct ttt aac	cag gag aga att	gtt gat gtt	768
Ser Ile Leu Asp Trp	Thr Ser Phe Asn	Gln Glu Arg Ile	Val Asp Val	
245	250	255		
gct gga cca ggg ggt	tgg aat gac cca	gat atg tta gtg	att ggc aac	816
Ala Gly Pro Gly Trp	Asn Asp Pro Asp	Met Leu Val Ile	Gly Asn	
260	265	270		
ttt ggc ctc agc tgg	aat cag caa gta	act cag atg gcc	ctc tgg gct	864
Phe Gly Leu Ser Trp	Asn Gln Gln Val	Thr Gln Met Ala	Leu Trp Ala	
275	280	285		

atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc 912
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300

cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat 960
 Pro Gln Ala Lys Ala Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

cag gac ccc ttg gcc aag caa ggg tac cag ctt aga cag gga gac aac 1008
 Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct 1056
 Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

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 Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc 1152
 Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act 1200
 Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag 1248
 Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

cta gaa aac aca atg tct gaa aag gac gaa tta tga 1284
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<211> 427

<212> PRT

<213> Homo sapiens

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 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met

	85		90		95										
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
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Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
	115						120						125		
Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
	130					135					140				
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
	145				150					155				160	
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
			165						170					175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
	180							185					190		
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
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Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
	210					215					220				
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys
	225				230					235				240	
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
			245					250					255		
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
			260					265				270			
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
	275					280						285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
	290					295					300				
Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
	305				310					315				320	
Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
			325					330					335		
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
	340						345					350			
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala
	355						360					365			
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile
	370					375					380				
Thr	Gln	Leu	Leu	Pro	Val	Lys	Arg	Lys	Leu	Gly	Phe	Tyr	Glu	Trp	Thr
	385				390					395				400	
Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu	Gln
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Leu	Glu	Asn	Thr	Met	Ser	Glu	Lys	Asp	Glu	Leu					
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<220>
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cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
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gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
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agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	
65 70 75 80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg	288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
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gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc	336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	
100 105 110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga	384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
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ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc	432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
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ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct	480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	
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Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	
165 170 175	
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Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	
180 185 190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	
195 200 205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	

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gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn 260 265 270			816
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala 275 280 285			864
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser 290 295 300			912
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn 305 310 315 320			960
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tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln 405 410 415			1248
cta taa Leu *			1254

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 <212> PRT
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<400> 16

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Asp	Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
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Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
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Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
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Trp	Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
				85				90						95	
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
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Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
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Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
		130					135					140			
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
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Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
				165					170					175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
				180				185						190	
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
				195				200				205			
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
				210			215					220			
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys
				225			230				235			240	
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
				245						250				255	
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
				260				265					270		
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
				275				280				285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
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Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
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Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
				325					330					335	
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
				340				345					350		
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala
				355			360					365			
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile

370 375 380
 Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
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<220>
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 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30
 gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag 144
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc 192
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc 240
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg 288
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag gcg 336
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110
 ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga 384
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125
 ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc 432
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140

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Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	
165 170 175	
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat	576
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	
180 185 190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	
195 200 205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	
210 215 220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag	720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys	
225 230 235 240	
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt	768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val	
245 250 255	
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac	816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn	
260 265 270	
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Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala	
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atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc	912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser	
290 295 300	
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat	960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn	
305 310 315 320	
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac	1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn	
325 330 335	
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct	1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala	
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Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala	

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Val Ala Ser Leu Gly Lys	Gly Val Ala Cys	Asn Pro Ala Cys Phe Ile	
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Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
385	390	395	400
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
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cta tct gaa aag gac gaa tta tga			1272
Leu Ser Glu Lys Asp Glu Leu *			
420			

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 <211> 423
 <212> PRT
 <213> Homo sapiens

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 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys

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225          230          235          240
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
          245          250          255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
          260          265          270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
          275          280          285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
          290          295          300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
          305          310          315          320
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
          325          330          335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
          340          345          350
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
          355          360          365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
          370          375          380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
          385          390          395          400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
          405          410          415
Leu Ser Glu Lys Asp Glu Leu
          420

<210> 19
<211> 1215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (10)...(1215)

<400> 19
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          1          5          10

ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg gac      99
Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp
          15          20          25          30

aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag cgc      147
Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
          35          40          45

ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc agt      195
Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
          50          55          60

gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc tgg      243
Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp

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65

70

75

aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg gct 291
 Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
 80 85 90

ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc ttt 339
 Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe
 95 100 105 110

cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga ctg 387
 Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu
 115 120 125

aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc ttc 435
 Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe
 130 135 140

cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct gac 483
 Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp
 145 150 155

tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt ttg 531
 Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu
 160 165 170

gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat agg 579
 Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg
 175 180 185 190

act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg tgg 627
 Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp
 195 200 205

ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat cac 675
 Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His
 210 215 220

tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag agt 723
 Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser
 225 230 235

atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt gct 771
 Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala
 240 245 250

gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac ttt 819
 Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe
 255 260 265 270

ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct atc 867
 Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile
 275 280 285

atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc cct 915
 Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
 290 295 300

caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat cag 963
 Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln
 305 310 315

gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac ttt 1011
 Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe
 320 325 330

gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct atg 1059
 Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met
 335 340 345 350

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 Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val
 355 360 365

gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc aca 1155
 Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr
 370 375 380

cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act tca 1203
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agg tta aga taa 1215
 Arg Leu Arg *
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 <211> 401
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Cys Asn Leu Asp Cys Gln Glu Pro Asp Ser Cys Ile Ser Glu Lys
 50 55 60
 Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp Lys Asp
 65 70 75 80
 Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala Pro Gln
 85 90 95
 Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe Pro His
 100 105 110
 Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys Leu

	115		120		125	
Gly	Ile Tyr Ala Asp Val	Gly	Asn Lys Thr Cys	Ala Gly Phe Pro Gly		
130		135		140		
Ser	Phe Gly Tyr Tyr Asp	Ile	Asp Ala Gln Thr	Phe Ala Asp Trp Gly		
145		150		155		160
Val	Asp Leu Leu Lys Phe	Asp Gly Cys Tyr	Cys Asp Ser Leu	Glu Asn		
	165		170		175	
Leu	Ala Asp Gly Tyr Lys	His Met Ser	Leu Ala Leu	Asn Arg Thr Gly		
	180		185		190	
Arg	Ser Ile Val Tyr Ser	Cys Glu Trp	Pro Leu Tyr	Met Trp Pro Phe		
	195		200		205	
Gln	Lys Pro Asn Tyr Thr	Glu Ile Arg	Gln Tyr Cys	Asn His Trp Arg		
	210		215		220	
Asn	Phe Ala Asp Ile Asp	Asp Ser Trp Lys	Ser Ile Lys	Ser Ile Leu		
225		230		235		240
Asp	Trp Thr Ser Phe	Asn Gln Glu Arg	Ile Val Asp	Val Ala Gly Pro		
	245		250		255	
Gly	Gly Trp Asn Asp Pro	Asp Met Leu	Val Ile Gly	Asn Phe Gly Leu		
	260		265		270	
Ser	Trp Asn Gln Gln Val	Thr Gln Met	Ala Leu Trp	Ala Ile Met Ala		
	275		280		285	
Ala	Pro Leu Phe Met Ser	Asn Asp Leu Arg	His Ile Ser	Pro Gln Ala		
	290		295		300	
Lys	Ala Leu Leu Gln Asp	Lys Asp Val Ile	Ala Ile Asn	Gln Asp Pro		
305		310		315		320
Leu	Gly Lys Gln Gly Tyr	Gln Leu Arg	Gln Gly Asp	Asn Phe Glu Val		
	325		330		335	
Trp	Glu Arg Pro Leu Ser	Gly Leu Ala Trp	Ala Val Ala	Met Ile Asn		
	340		345		350	
Arg	Gln Glu Ile Gly Gly	Pro Arg Ser Tyr	Thr Ile Ala	Val Ala Ser		
	355		360		365	
Leu	Gly Lys Gly Val Ala	Cys Asn Pro	Ala Cys Phe	Ile Thr Gln Leu		
	370		375		380	
Leu	Pro Val Lys Arg Lys	Leu Gly Phe Tyr	Glu Trp Thr	Ser Arg Leu		
385		390		395		400
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 <213> Homo sapiens

<220>
 <221> CDS
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cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	

20

25

30

gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag 144
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc 192
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60

agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc 240
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80

tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg 288
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95

gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc 336
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110

ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga 384
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125

ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc 432
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140

ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct 480
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160

gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt 528
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175

ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat 576
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190

agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg 624
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205

tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat 672
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220

cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag 720
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240

agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val 245 250 255	768
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn 260 265 270	816
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala 275 280 285	864
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser 290 295 300	912
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn 305 310 315 320	960
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atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala 355 360 365	1104
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aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr 385 390 395 400	1200
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<211> 409	
<212> PRT	
<213> Homo sapiens	
<400> 22	
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Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp	

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Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg						
	35		40		45	
Phe Met Cys Asn Leu Asp Cys Gln Glu Pro Asp Ser Cys Ile Ser						
	50		55		60	
Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp						
	65		70		75	
Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala						
	85		90		95	
Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe						
	100		105		110	
Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu						
	115		120		125	
Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe						
	130		135		140	
Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp						
	145		150		155	
Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu						
	165		170		175	
Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg						
	180		185		190	
Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp						
	195		200		205	
Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His						
	210		215		220	
Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser						
	225		230		235	
Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala						
	245		250		255	
Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe						
	260		265		270	
Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile						
	275		280		285	
Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro						
	290		295		300	
Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln						
	305		310		315	
Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe						
	325		330		335	
Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met						
	340		345		350	
Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val						
	355		360		365	
Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr						
	370		375		380	
Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser						
	385		390		395	
Arg Leu Arg Ser Glu Lys Asp Glu Leu						
	405					

<210> 23

<211> 30

<212> PRT

<213> Tobacco mosaic virus

<400> 23

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Gln	Leu	Glu	Asn	Thr	Met	Gln	Met	Ser	Leu	Lys	Asp	Leu	Leu		
			20					25					30		

<210> 24

<211> 36

<212> PRT

<213> Tobacco mosaic virus

<400> 24

Thr	Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu
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Gln	Leu	Glu	Asn	Thr	Met	Gln	Met	Ser	Leu	Lys	Asp	Leu	Leu	Ser	Glu
			20					25					30		
Lys	Asp	Glu	Leu												
			35												

<210> 25

<211> 26

<212> PRT

<213> Tobacco mosaic virus

<400> 25

Thr	Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu
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Gln	Leu	Glu	Asn	Thr	Met	Gln	Met	Ser	Leu						
			20					25							

<210> 26

<211> 32

<212> PRT

<213> Tobacco mosaic virus

<400> 26

Thr	Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu
1				5					10					15	
Gln	Leu	Glu	Asn	Thr	Met	Gln	Met	Ser	Leu	Ser	Glu	Lys	Asp	Glu	Leu
			20					25					30		

<210> 27

<211> 22

<212> PRT

<213> Tobacco mosaic virus

<400> 27

Thr	Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu
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Gln	Leu	Glu	Asn	Thr	Met										
			20												

<210> 28

<211> 29
 <212> PRT
 <213> Tobacco mosaic virus

<400> 28
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<210> 29
 <211> 18
 <212> PRT
 <213> Tobacco mosaic virus

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<210> 30
 <211> 24
 <212> PRT
 <213> Tobacco mosaic virus

<400> 30
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 1 5 10 15
 Gln Leu Ser Glu Lys Asp Glu Leu
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<210> 31
 <211> 5
 <212> PRT
 <213> Tobacco mosaic virus

<400> 31
 Thr Ser Arg Leu Arg
 1 5

<210> 32
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 <213> Tobacco mosaic virus

<400> 32
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<210> 33
 <211> 11641
 <212> DNA
 <213> Tobacco mosaic virus

<400> 33

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<212> PRT

<213> Tobacco mosaic virus

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Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr

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<212> PRT

<213> Rice

<400> 37

Ser Glu Lys Asp Glu Leu

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